FIGURE 1A

```
1    GNTCTAGAAN TAGTGGATCC CCCGGGCTG  CAGGAATTCC GGAAGGGCTC TGGTGGGGCT GACGGCCCCT CCCGCGGGGC CCGCGGGGGC
     CNAGATCTTN ATCACCTAGG GGGCCCGAC  GTCCTTAAGG CCTTCCCGAG ACCACCCCGA CTGCGGGGGA GGGCGCCCCG CGGCCCCGTC

101  CAGGAAGCAG GTCCGCGTGG GCGCTGGGG  CGGGGTGGTC CGGGGCTGAAG AGCCAGGCAG CCAAGGCAGC CACCCCGGGG GGTGGGCGAC
     GTCCTTCGTC CAGGCGCACC CGCGACCCCC GCGCCCCACC GCCCCGACTTC TCGGTCCGTC GGTTCCGTCG GTGGGGCCCC CCACCCGCTG

201  TTTGGGGGAG TTGGTGCCCC GCCCCCCAGG CCTTGGCGGG GTCATGGGGC TGGGGCCCGGG CCCCCCATTC TGGGCCCGGGG TCGGGGCCCT GCTGCTGCTG
     AAACCCCCTC AACCACGGGG CGGGGGGTCC GGAACCGCCC CAGTACCCCG GGGGGGTAAG  CCCGGGGTAAG ACCCCGGGGC AGCCCCGGGA CGACGACGAC
  1                                                               MetGlyP  roProHisSe  rGlyProGly  aLeuLeuLeu

301  GGGGTTTTGG GGCTGGTGTC TGGGCTCAGC CTGGAGCCTG TCTACTGGAA CTCGGCGAAT AAGAGGTTCC AGGCAGAGGG TGGTTATGTG CTGTACCCTC
     CCCCAAAACC CCGAGTCG   ACCGAGTCG  GACCTCGGAC AGATGACCTT GAGCGCCTTA TTCTCCAAGG TCCGTCTCCC ACCAATACAC GACATGGGAG
  20 GlyValLeuG  lyLeuValSe  rGlyLeuPro V  leGluProV  alTyrTrpAs  nSerAlaAsn  LysArgPheG  lnAlaGluGl  yGlyTyrVal  LeuTyrProGln

401  AGATCGGGGA CCGGCTAGAC CTGCTCTGCC CCCGGGCCCG GGACCCCGGGA GGACCCCGGGA TGAGTTCTAC AAGTCGTACC TGGTAGGGGG
     TCTAGCCCCT GGCCGATCTG GACGAGACGG GGGCCCGGGC CCTGGGGCCCT CCTGGGGCCCT ACTCAAGATG TTCGACATGG ACCATCCCCC
  54 IleGlyAs   pArgLeuAsp  LeuLeuCysP  roArgAlaAr  gProProGly  gProProGly  erProAsnTy  rGluPheTyr  LysLeuTyrL  euValGlyGly

501  TGCTCAGGGC CGGCGCTGTG AGGCACCCCC TGCCCCAAAC CTCCTTCTCA CTTGTGATCG CCCAGACCTG GATCTCCGCT GTTCCAGGAG
     ACGAGTCCCG GCCGCGACAC TCCGTGGGGG ACGGGGTTTG GAGGAAGAGT GAACACTGAC GGGTCTGGAC CTAGAGGCGA CAAGGTCCTC
  87 AlaGlnGly   ArgArgCysG  luAlaProPr  oAlaProAsn  LeuLeuLeuT  hrCysAspAr  gProAspLeu  AspLeuArgP  heThrIleLy  sPheGlnGlu

601  TATAGCCCTA ATCTCTGGGG CCACGAGTTC CGCTCGCACC ACGATTACTA CATCATTGCC GAGGGGCTGT GGACCCGGGA AAATGCCCAT
     ATATCGGGGA TAGAGACCCC GGTGCTCAAG GCGAGCGTGG TGCTAATGAT GTAGTAACGG CTCCCCGACA CCTGGGGCCT TTTACGGGTA
  120 TyrSerProA  snLeuTrpGl  yHisGluPhe  ArgSerHisH  isAspTyrTy  rIleIleAla  GluGlyLeu  lyThrArgGl  uAsnAlaHis

701  GAGGTGTGTG CCTAACCAGA TGCTTCTCCG AGTGGGACAA AGTCCCCGAG GGACCCGGGA CCTGTGTCTG CCCGGGGTGC TGAAGGCCCC
     CTCCACACAC GGATTGGTCT ACGAAGAGGC TCACCCTGTT TCAGGGGCTC CCTGGGGCCT GGACACAGAC ACTTCCGGGG
  154 GlyValCy    sLeuThrArg  CysPheSerV  alGlyGln   SerProArgG  lyProArgG  lyLeuGluLe  uSerLeuGlnGly

801  GGAAAGAGAC CGAGGGGCAG CCCACCAGCC GGAGCCTGGG AAGGAGAACC TGCCAGGTGA CCCCACCAGC AATGCAACCT CCCGGGGTGC TGAAGGCCCC
     CCTTTCTCTG GCTCCCCGTC GGGTGTCGGA CCTCGGACCC TTCCTCTTGG ACGGTCCACT GGGGTGGTCG TTACGTTGGA GGGCCCCACG ACTTCCGGGG
  187 GluArgAsp   ArgGlyAlaA  laHisSerLe  uGluProGly  LysGluAsnL  euProGlyAs  pProThrSer  AsnAlaThrS  erArgGlyAl  aGluGlyPro

901  CTGCCCCCTC CCAGCATGCC TGCAGTGGCT GGGGCAGCAG GGGGGCTGGG GCTGCTCTTG CAGGGGCTGG GGTTGGCGGA
     GACGGGGGAG GGTCGTACGG ACGTCACCGA CCCCGTCGTC CCCCGACCCC CGACGAGAAC GTCCCCGACC CCAACCGCCT
  220 LeuProProP  roSerMetPr  oAlaValAla  GlyAlaAlaG  lyGlyLeuVal AlaLeuLeuLeu aLeuGlyLeuVal aLaGlyAlaMet CysTrpArgArg

1001 GACGGCGGGC CAAGCCTTCG GAGAGTCGCC ACCCTGGTCC TGGCTCCTTC GGTCTCTGGG CCTGGGGGGT GGAGGTGGGA TGGGACCTCG
     CTGCCGCCCG GTTCGGAAGC CTCTCAGCGG TGGTGGGACC ACCGAGGAAG CCAGAGACCC GGACCCCCCA CCTCCACCCT ACCCTGGAGC
  254 ArgArgAl    aLysProSer  GluSerArgH  isProGlyPr  oGlySerPhe  GlyLeuLeuG  lyLeuGlyGly  lyGlyGlyGlyM etGlyProArg

1101 GGAGGCTGAG CCTGGGGGT  TAGGGATAGC TCTGCGGGGG CAGATCCCCC CTTCTGCCCC CACTATGAGA AGGTGAGTGG TGACTATGGG
     CCTCCGACTC GGACCCCCCA ATCCCTATCG AGACGCCCTG GTCTAGGGGG GAAGACGGGG GTGATACTCT TCCACTCACC ACTGATACCC
  287 GluAlaGlu   ProGlyGluL  euGlyIleAl  aLeuArgGly  laAspProPr  oPheCysPro  oHisTyrGluL ysValSerGl  yAspTyrGly
```

FIGURE 1B

```
1201 CATCCTGTGT ATATCGTGCA GGATGGGCCC CCCCAGAGCC CTCCAAACAT CTACTACACA TCGATTTCTG TGTTGGAGTG GCCCATATTG CATACGATAC
     GTAGGACACA TATAGCACGT CCTACCCGGG GGGGTCTCGG GAGGTTTGTA GATGATGTGT AGCTAAAGAC ACAACCTCAC CGGGTATAAC GTATGCTATG
320  HisProValT yrIleValGl nAspGlyPro ProGlnSerP roProAsnIl eTyrTyrThr SerIleSerV alLeuGluTr pProIleLeu HisThrIleGln

1301 AACTGTTTTT CATGCGATCC AAGTGCTCCC GTGTCACTAC ATTCTTATTT CCTGTGCAAG TTATTACGAC ATCGACTTGC CGGATGACTT CATTTAGCTT
     TTGACAAAAA GTACGCTAGG TTCACGAGGG CACAGTGATG TAAGAATAAA GGACACGTTC AATAATGCTG TAGCTGAACG GCCTACTGAA GTAAATCGAA
354  LeuPhePh eMetArgSer LysCysSerA rgValThrTh rPheLeuPhe ProValGlnV alIleThrTh rSerThrCys ArgMetThrS erPheSerPhe

1401 TACCACCCTG AACCCATCCA TGCAGGCCTG CAGAGCACAG ATGGGGGGAAT TCCGAATCAG ATGGTGTTTC TGGGGGGACA GGATCCTGGG TACGGCTCTG
     ATGGTGGGAC TTGGGTAGT ACGTCCGGAC GTCTCGTGTC TACCCCCTTA AGGCTTAGTC TACCACAAAG ACCCCCCTGT CCTAGGACCC ATGCCGAGAC
387  ThrThrLeu AsnProSerM etGlnAlaCy sArgAlaGln MetGlyGluP heArgIleAr gTrpCysPhe rgIleLeuGl yThrAlaLeu

1501 TTTGTGCTTG TCTTCTTGGG AGGCTGAATA TGCATCAGAC GACACTGCTC CGGCAACGGG CCAGTGTGGA GGCGGAAGCC GGCCAGCATG
     AAACACGAAC AGAAGAACCC TCCGACTTAT ACGTAGTCTG CTGTGACGAG GCCGTTGCCC GGTCACACCT CCGCCTTCGG CCGGTCGTAC
420  PheValLeuV alLeuIleLe uLeuLeuGly ArgLeuAsnM etHisGlnTh rThrLeuLeu ArgGlnArgA laSerValGl uAlaGluAla GlyGlnHisGly

1601 GTCCCCTGTG ATAGGATTGA AAGAGCTACT GAGAATAGGG GGCTTCTCAA TGAGAGAGCG TTATCATGGG AACCAGGCAG ATCAATCATC
     CAGGGGACAC TATCCTAACT TTCTCGATGA CTCTTATCCC CCGAAGAGTT ACTCTCTCGC AATAGTACCC TTGGTCCGTC TAGTTAGTAG
454  ProLeu

1701 CCTGGCCAGT CAGGCAGGAA GTTACTTAGC TTCTCCTTCA CCTTCTTCCC ACAGAATTTA TTATAGGCTT GTTCCAAGTT GTAGTGTGTG ATCAGATTCG
     GGACCGGTCA GTCCGTCCTT CAATGAATCG AAGAGGAAGT GGAAGAAGGG TGTCTTAAAT AATATCCGAA CAAGGTTCAA CATCACACAC TAGTCTAAGC

1801 TGCTGCCTGT CAGCTCTGTG CTACCTGGCA GTTCCCCTCA TGGAATTCGA TATCAAGCTT ATCGATACCG TCGACCT
     ACGACGGACA GTCGAGACAC GATGGACCGT CAAGGGGAGT ACCTTAAGCT ATAGTTCGAA TAGCTATGGC AGCTGGA
```

FIGURE 2A

```
1     GNTCTAGAAN TACTCGATCC CCCCGGGCTG CAGGAATTCC GACCCCCCCT GGAAGGGCTC TGGTGGGGCT GACCCCCCCT CCCCGGGGGC GCGGGCACAG
      CNAGATCTTN ATCACCTAGG GGGGCCCGAC GTCCTTAAGG CTGCCGGGGA CCTTCCCGAG ACCACCCCGA CTGGGGGGGA GGGGCCCCCG CGCCCGTGTC

101   CACGAAGCAG GTCCCCCTGG GCGCTGGGGG CATCAGCTAC CGGGGCTGTC CGGGCTGAAC AGCCAGGCAG CCAAGGCAGC CACCCCCGGG GGTGGGGCGAC
      GTCCTTCGTC CAGGGGGACC CKCGACXCCC GTAGTCGATG GCCCCACCAG TCGGTCCGTC GGTCCGGTCG

201   TTTGGCGGAC CCTTGGCGGG GCCCCTCGCC GTCATGGGGC CCCCCCATTC TGGGCCGGGG TCGGGCCCGG GCTGCTGCTG
      AAACCCCCTC AACCACGGGG CGGGGGGTCC GGAACCGGCC CAGTACCCCG GGGGGGTAAG ACCCGGCCCC AGCCCGGGGA CCAGGACGAC
1                                    MetGlyP   roProIlSe  rGlyProGly GlyValAArgv  uLeuLeuLeu

301   GGGGTTTGG  GGCTGGTGTC TGGGCTCAGC CTGGAGCCTG AAGAGGTTCC CTCGGGGAAT AGGCAGAGGG TGGTTATGTG CCGTACCCTC
      CCCAAAAGCC CCGACCACAG ACCCGAGTCG GACCTGGGAC AGATGAICTT TTCTTCCAGG TCCGGGGCTTA ACCAATATAC GACATGGGAG
20    GlyValLrvG  lylLeuVLSe  rGlyLeuSer  LeuGluProv  LysArgPheG  lnAlaGluGl  yGlyTyrVal  LeuTyrProGln

401   AGATCGGGGA CCGGCTAGAC CTGCCTCRCC CCCGGGGCCCC GCCTCCTGGC CTCCACTCCT CTCCTAATTA TGAGTTCTAC AAGCTGTACC TGGTAGGGGC
      TCTAGCCCCT GGCCGATCTG GACGAGACGG GGGCCCGGGG CGGAGGACCG GGAGGACGCG GGGATTAAT ACTCAAGATG TTCGAACATGG ACCATCCCCG
54    IleGlyAs   pArgLeuAsp  LeuLeuCysP  roArgAlaAr  rGluArgPheG  ProProGly  ProHisSerS  erProAsnTy  rGluPheTyr  LysLeuTyrL  euValGlyGly

501   TGCTCAGGGC CGGCCCTGTG AGGCACCCCC TGCCCCAAAC CTTGTGAGGCG GATCCTCGCT TCACCATCAA GTTCCAGGAC
      ACGAGCCCCG GCCGGGACAC TCCGTGGGGG ACGGGGTTTG GGGGAAGAGT CCCGGACCTG CTAGAGGCGA AGTGGTAGTT CAAGGTCCTC
87    AlaGlnGly  ArgArgCysG  luAlaProPr  oAlaProAsn  LeuLeuLeuP  rProAspPeu  gProxAspAr  AspLeuArgP  heThrIleLy  sPheGlnGlu

601   TATAGCCCTA ATCTCTGGGG CCTAACCAGA CGCTCGCACC ACGATTACTA CATCATTGCC ACATGGGATG GGGCCTGGGA AGCCTGGAGG
      ATATCGGGAT TAGAGACCCC GGATTGGTCT GCGAGCGTGG GCTAATGAT GTAGTAACGG GTGTACCCTAC CCCGGACCCT TCGGACTTT
120   TyrSerProA  snleuTrpG  lySerProA  rgSerHisH  isAspTyrTy  rIleIleAla  ThrGlyAsp  GlyAlaTrp  uGlyLeuGlu  SerLeuGlnGly

701   GGAGTGTGTG CCTAACCAGA GGCATGAAGG TCCTTCTCCC AGTGGGACAA AGTCCCGAG ACATGGGATG GGGCCTGGGA CCTGTGTCTG AAATGCCCAT
      CCCACACAC GGATTGGTCT CCGTACTTCC TGCTCCTTCC ACGAGAGGC TCACCGGTT GTAGTAACGG CCCGGACCCTC GGACACAGAC TTTACGGGTA
154   GlyValACy  sLeuThrArg  GlyMetLysv  alLeuLeuAr  gValGlyGlu  SerProArgG  lyGlyAlaVa  ThrSerAspG  lyProArgly  lPheArglys  luMetProMet

801   GGAAAGAGAC CGAGGGGCAG CCCACAGCCT GGAGCCTGCA AAGGAGAACC TGCCAGGTCA CCCACCAGC AATGCAACCT CCCGGGGTGC
      CCTTCTCTG GCTCCCCGTC GGGTGTCGGA AGGAGCCCCTTG TTCCTCTTGG ACGGTCCAGT GGGTGGTTCG TTACGTTGGA GGGCCCCACG
187   GluArgAsp  ArgGlyAlaA  laHisSerLe  uGluProGly  LysGluAsnL  euProGlyAs  pProThrSer  AsnAlaThrS  erArgGlyAl  aGluGlyPro

901   CTGCCCCCTC CCAGCATGCC TGCAGTGGCT GCGGGCTGCG GGGGCTCTTC GCTGCTCTTC CAGGGCGTGG GGTGCCCATG TGTTGCCGGA
      GACGGGGGAG GGTCGTACGG ACGTCACCGA CGCCCGACGC CCCCGACGAC GACGAGAAAC GTCCCGCACC CCACGGGTAC ACAACGGCCT
220   LeuProProp  roSerMetPr  oAlaValAla  GlyAlaLeuAl  aLeuLeuLeu  LeuGlyLeuL  aLeuGlyLeuVal  aLaGlyAlaGl  yGlyAlaMet

1001  GACGGGGGGC CAAGCCTTCG GAGAGTCGCC ACCCTGGTCC TGGCTCCTTC CGGAGGGGAG GGTCTCTGGG CCTGGGGGGT GGAGGTCGGA CCTGGGCCTG
      CTGCCCCCCG GTTCGGAAGC CTCTCAGCGG TGGGACCAGG ACCGAGGAAG GCCTCCCCTC CCAGAGACCC GGACCCCCCA GGACCCGGAC CCTKKACCCT
254   ArgArgAl   aLysProSer  GluSerArgH  isProGlyPr  oGlySerPhe  GlyArgGlyC  lySerLeuG  lyLeuGlyGl  yLeuGlyGly  GlyGlyGlyM  etGlyProAr
```

FIGURE 2B

```
1101 GGAGGCTGAG CCTGGGGAGC TAGGGATAGC TCTGCGGGGGT GGCGGGGGCTG CAGATCCCCC CTTCTGCCCC CACTATGAGA AGGTCAGTGG TGACTATGGG
     CCTCCGACTC GGACCCCTCG ATCCCTATCG AGACGCCCCA CCGCCCCGAC GTCTAGGGGG GAAGACGGGG GTGATACTCT TCCACTCACC ACTGATACCC
287  GluAlaGlu ProGlyGluL euGlyIleAl aLeuArgGly GlyGlyGlyAlaa laAspProPr oPheCysPro HisTyrGluL ysValSerGl yAspTyrGly

1201 CATCCCTGTGT ATATCGTGCA GGATGGGCCC CCCCAGAGCC CTTCCAAACAT CTACTACAAG GTATGAGGGC TCCTCTCACG TGGCTATCCT GAATCCAGCC
     GTAGGACACA TATAGCACGT CCTACCCGGG GGGGTCTCGG GAGGTTTGTA GATGATGTTC CATACTCCCG AGGAGAGTGC ACCGATAGGA CTTAGGTCGG
320  HisProValT yrIleValGl nAspGlyPro ProGlnSerP roProAsnIl eTyrTyrLys ValOP*

1301 CTTCTTGGGG TGCTCCTCCA GTTTAATTCC TGGTTTGAGG GACACCTCTA ACATCTCGGC CCCCTGTGCC CCCCCAGCCC CTTCACTCCT CCCGGCTGCT
     GAAGAACCCC ACGAGGAGGT CAAATTAAGG ACCAAACTCC CTGTGGGAT TGTAGAGCCG GGGGACACGG GGGGTCGGG GAAGTGAGGA GGGCCGACGA

1401 GTCCCGTCT CCACTTTAG GATTCCTTAG GATTCCCACT GCCCCCACTTC CTGCCCCTCC GTTTGGCCAT GGGTGCCCCC CTCTGTCTCA GTGTCCCTGG
     CAGGAGCAGA GGTGAAATC CTAAGGAATC CTAAGGGTGA GACGGGAGGG CAAACCGGTA CCCACGGGGG GAGACAGAGT CACAGGGACC

1501 ATCCTTTTTC CTTGGGGAGG GGCACAGGCT CAGCCTCCTC TCTGACCATC ACCCAGCCAT CCTTGTCCCC CTCACCCACC CAGAGCTAGG GGCGGGAACA
     TAGGAAAAG GAACCCCTCC CCGTGTCCGA GTCGGAGGAG AGACTGGTAC TGGGTCCGTA GGAACAGGGG GTCTCGATCC CCGCCCCTTGT

1601 GCCCACCTTT TGGTTGGCAC CGCCTTCTTT CTGCCTCTCA CTGGTTTTCT CTTCTTCTATC TCTTATTCTT CCGTCTCTAG GTCTGTTCTT
     CGGGTGGAAA ACCAACCGTG GCGGAAGAAA GACGGAGAGT GACCAAAAGA GAAGAGATAG AGAATAAGAA AGGGAGAGAA GGCAGAGATC CAGACAAGAA

1701 CTTCCCCTAGC ATCCTCCTCC CCACATCTCC TTTCACCCTC TTGGCTTCTT ATCCTGTGCC TCTCCCATCT CCTGGGTGGG GGCATCAAAG CATTCTCCCC
     GAAGGGATCG TAGGAGGAGG GGTGTAGAGG AAAGTGGGAG AACCGAGAA TAGGACACGG AGAGGGTAGA CCCTAGTTTC GTAAACAGGG

1801 CTTAGCTTTC AGCCCCCCTT CTGACCTCTC ATACCAACCA CTCCCCCTCAG TCTGCCCAAAA ATGGGGGCCT TATGGGGAAG GCTCTGACAC TCCACCCCAG
     GAATCGAAAG TCGGGGGGAA GACTGGAGAG TATGGTTGGT GAGGGGAGTC AGACGGTTTT TACCCCCGGA ATACCCCTTC CGAGACTGTG AGGTGGGGTC

1901 CTCAGGCCAT GGGCACCAGG GCTCCATTCT CTGGCCTGGC CCAGGCCTCT ACATACTTAC TCCAGCCATT GGGTCATGAC AGCTACCATG
     GAGTCCGGTA CCCGTCGTCC CGAGGTAAGA GACCGGACCG GGTCCGGAGA TGTATGAATG AGGTCGGTAA ACCCCACCAA CCCAGTACTG TCGATGGTAC

2001 AGAAGAAGTG TCCCGTTTTC TCCACTGGCC AATAGCAAGA TATGAACCGG TCGGGGACATG TATGGACTTG GTCTCATGCT GAATGGGCCA CTTGGGACCG
     TCTTCTTCAC AGGGCAAAAC AGGTCACCGG TTATCGTTCT ATACTTGGCC AGCCCTGTAC CAGACTACGA CTTACCCGGT GAACCCTGGC

2101 GAAGTGACTT GCTCCAGACA AGAGGTGACC AGGCCCGGAC TGGGAAGTAG CAGAAGCAGT GCAGCAGGAA CTGGAAGTGC CTTCATCCAG
     CTTCACTGAA CGAGGTCTGT TCTCCACTGG TCCGGGCCTG TCTTTACCGG ACCTTCATC GTCTTCGTCA CGTCGTCCTT GACCTTCACG GAAGTAGTC

2201 GACAGGAAGT AGCACTTCTG AAACAGGAAG TGGTCTGGCT GGAACTCCAA GTGGCTTAGT CTGGGGGATC AGGAGGTGGG AGGTGGATGG TTCTTATTCT
     CTGTCCTTCA TCGTGAAGAC TTTGTCCTTC ACCAGACCGA CCTTGAGGTT CACCGAATCA GACCCCCTAG TCCTCCACCC TCCACCTACC AAGAATAAGA

2301 GTGGAGAAGA AGGGCGGGAA GAACTTCCTT TCAGGAGGAA GCTGGAACTT ACTGACTGTA AGAGGTTAGA GGTGGACCGA
     CACCCTCTCA TCCCGCCCTT CTTGAAGGAA AGTCCTCCTT CGACCTTGAA TGACTGACAT TCTCCAATCT CCACTGGCT
```

FIGURE 3A

```
AL-2b.L        . GTTCTAGAANTAGTGGATCCCCCCGGGCTGCAGGAATTCCGACGGCCCT
AL-2b.L     51 GGAAGGGCTCTGGTGGGGCTGAGCGCTCTGCCGCGGGGCGCGGGGAGAG
AL-2b.L    101 CAGGAAGCAGGTCCGCGTGGGCGCTGGGGGCATCAGCTACCGGGGTGGTC
AL-2b.L    151 CGGGCTGAAGAGCCAGGCAGCCAAGGCAGCCACCCCGGGGGGTGGGCGAC
AL-2b.L    201 TTTGGGGGAGTTGGTGCCCCGCCCCCCAGGGGTTGGCGGGGTCATGGGGC
AL-2b.L    251 CCCCCCATTCTGGGCCGGGGGGGCGTGCGAGTCGGGGCCCTGCTGGTGCTG
AL-2b.L    301 GGGGTTTTGGGGGCTGGTGTCTGGGCTCAGCCTGGAGCCTGTCTACTGGAA
AL-2b.L    351 CTCGGCGAATAAGAGGTTCCAGGCAGAGGGTGGTTATGTGCTGTACCCTC
AL-2b.L    401 AGATCGGGGACCGGGTAGACCTGCTCTGCCCCCGGGGCCGGGCTCCTGGC
AL-2b.L    451 CCTCACTCCTCTCCTAATTATGAGTTCTACAAGCTGTAGCTGGTAGGGGG
AL-2b.L    501 TGCTCAGG GCCGG CGGTGTGAGGCACCCCCTGGGCCAAACCTCCTTCTCA
H10006       1 ........ GCCGA CGGTGTGAGGCACCCCCTGCCCCAAACCTCCTTCTCA

AL-2b.L    551 CTTGTGATCGCCCAGACCTGGATCTCCGCTTCACCATCAAGTTCCAGGAG
H10006      43 CTTGTGATCGCCCAGACCTGGATCTCCGCTTCACCATCAAGTTCCAGGAG

AL-2b.L    601 TATAGCCCTAATGTGTGGGGCGGACGAGTTCCGGCTCGCACCACGATTACTA
H10006      93 TATAGCCCTAATGTGTGGGGCCCACGAGTTCCGGCTCGCACCACGATTACTA

AL-2b.L    652 CATCATTGCCACATCGGATGGGACCCGGGGAGG G CCT GGAGAGCCTGCAGG
H10006     143 CATCATTCCCACATCGGATGGGACCCGGGAGG C CTG GGAGAGCCTGCAGG

AL-2b.L    702 GA G GTGTGTGCCTAACCAGAGGCATGAAGGTGCTTCTCCGAGTG GGACAA
H10006     193 GA A GTGTGTGCCTAACCAGAGGCATGAAGGTGCTTCTCCGAGTN GGACAA

AL-2b.L    752 AGTC CCCGAGGAGGGGGCTGTCCCCCGAAAAACCTGTGTCTGAAATGCCCAT
H10006     243 AGT. CCCGAGGAGGGGGCTGTCCCCCGAAAAACCT GTGTCTGAAATGCCCAT

AL-2b.L    801 GGAAAGAGACCGAGGGGCAGCCCACAGCCT. GGAGCCT. GGGAAGGAGAA
H10006     293 GGAAAGAGACCGAGGGGCAGCCCACAGCCT GGAGCCT GGGAAGGAGAA

AL-2b.L    849 CCTGCCAGGTGACCCCACCAGCAAT G CAACCTC CCGGGGT. .CC TGAAGG
H10006     342 CCTGCCAGGTGACCCCACCAGCAAT N CAACCTT CCGGGGT TGCT TGAAGG

AL-2b.L    897 C CCCC . . G CCC CT CCCAGCA TGC TGCA GT . GGCT GGGCAGCAG G
H10006     392 G CCCCT TGA CCC TT CCCAGCA TTGC NTGCA NT GGTT N GGGGCAGCA NG

AL-2b.L    942 GGGG . . . . TGGC GCTGCTCTTGCTGGGCGTGGCAGGGCCTGGGGGTGCC
H10006     442 GGGG N GTTT TGGC

AL-2b.L    998 ATGTGTTGGCGGAGACGGCGGGCCAAGCCTTCGGAGAGTCGCCACCCTGG
AL-2b.L   1038 TCCTGGCTCCTTCGGGAGGGGAGGGTCTCTGGGCCTGGGGGGTGGAGGTG
AL-2b.L   1088 GGATGGGACCTCGGGCAGCTGAGCCTGGGGAGCTAGGGATAGGTCTGCGG
AL-2b.L   1138 GGTGGCGGGGCTGCAGATCCCCCCTTCTGCGGGCACTATGAGAAGGTGAG
```

AL-2b.L 1189 TGGTGACTA ⬤ GCATCC T GTGTATA T CGTGCAGGATG ⬤ CCCCCAGA

AL-2b.L 1233 GCCCTCCAAACATCTACTACACATCGATT T CTGTGTTGGAGTGGCCCATA

AL-2b.L 1283 TTGCAT T CGATACAACTGTT T TTCATGCGATCCAAGTGCTGCCGTGTCAC

AL-2b.L 1338 TACATTC T TATT T CCTGTGCAAGTTATTACGACATCGACTTGCCGGATGA

AL-2b.L 1388 CTTCATTTAGCTTTACGACCCTGAACCCATCCATGCAGGCCTGCAGAGCA

AL-2b.L 1438 CAGATGGGGGAATTCCGGAATCAGATGGTGT T TCTGGGGGGACAGGATCCT

AL-2b.L 1488 GGGTACGGCTC T GTTTGTGCTTGTGCTTATTCTTCTTCTTGGGAGGCTGA

AL-2b.L 1538 ATATGCATCAGACGACACTGCTCCGGCAACGGGCCAGTGTGGAGGCGGAA

AL-2b.L 1588 GCCGGCCAGCATGGTCCCCTGTGATAGGATTGAAAGAGCTACTGAGAATA

AL-2b.L 1638 GGGGCCTTCTCAATGAGAGAGCGCAGGCTGCTGTTATCATGGGAACCAGG

AL-2b.L 1688 CAGATCAATCATCCCTGGCAGGTCAGGCAGGAAGTTACTTAGCTTCTCCT

AL-2b.L 1738 TCACCTTCTTCCCACAGAATTTATTATAGGCTTGTTCCAAG T TGTAGTGT

AL-2b.L 1788 GTGATCAGATTCG T GCTGCCTGTCAGCTCTGTGCTACC T GGCAGTTCCCC

AL-2b.L 1838 TCATGGAATTCGATATCAAGCTTATCGATACCGTCGACCT

FIGURE 3B

```
lerk2     2  MA.RPGQRW    WLVAMVVWALCFLATPLA KNLEFVSW    NPKFLSGKG
huHTKL    1  MAVRRDSYW KYCWGVLNV---LCRTAISKSIV LEFIYWKSSVSKFLPQQG
AL2.sht   1  VG.PPHSGPGGVRVGALLLLGVLGLVSGL.SLEPVYWNSANKRFOAEGG
AL2.long  1  MG.PPHSGPGGVRVGALLLLGVLGLVSGL.SLEPVYWNSANKRFOAEGG

lerk2     52 .VIYPKIGDKLDIICPRA---EAGR..PYEYYKLYLVRPEOAAACSTVLC
huHTKL    48 LVLYPQIGDKLDIICP KV---DSKTVGQ YEYYKYMVCKDQADRCT..KKE.
AL2.sht   48 YVLYPQIGDRLDLLCPRARPPGPHSGPNYEFYKLYLVGGAQGRRCEAPPA
AL2.long  49 YVLYPQIGDRLDLLCPRARPPGPHSGPNYEFYKLYLVGGAQGRRCEAPPA

lerk2     95 PNVLVTCNAPEEIRFTIKFQEFSPNYMGLEFKKHGYYIITSTENGSLEG
huHTKL    95 NTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFCKNKDYYIISTSNGSLEG
AL2.sht   96 PNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG
AL2.long  96 PNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG

lerk2     145 LENREGGVCRTRTMKIIMKVCODPNAVTPEQLTTSRPSKEADNTVKMATQ
huHTKL    145 LDNQEGGVCQTRAMKILMKVGQQASB......AGSTRNKCPTRRPELEAG
AL2.sht   148 LESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVEEMPMERDRGAAHSLE
AL2.long  148 LESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVGEMPMERDRGAAHSLE

lerk2     195 APGSRGSLQDSDGKHETVNCEEKSGPGASGGSGDPDGFFHSKVALFAAV
huHTKL    199 TNG.RSSTTSPFVKPNPGSSTDQNSAGHSG.......NNILGSEVALFAG I
AL2.sht   198 .PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL...ALLLLGVA
AL2.long  198 .PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL...ALLLLGVA

lerk2     245 GAGCVIFLLIIIFLTVLLKLRKRHRKHTQ-QRAAALSLSTLASPKGGSG
huHTKL    273 ASGCIIFIVIIITLVVLLKYRRRHRKHSP-QHTTLSLSTLAITPKRSGN
AL2.sht   244 GAGGA....MCWRRRAKPSEERHPGPGGFGRGGSLGLGG....GGGMG
AL2.long  244 GAGGA....MCWRRRAKPSESRHPGPGSFGRGGSLGLGG....GGGMG

lerk2     294 TAGTEPSDIIIPLR...TTENNYCPHYEKVSGCYGHPVYIVOEMPPQSPA
huHTKL    282 NNGSEPSDIIIPLR...TADSYFCPHYEKVSGCYGHPVYIVOEMPPQSPA
AL2.sht   285 PREAEPGELGIALRGGGAADFPFCPHYEKVSGCYGHPVYIVODGPPQSPP
AL2.long  205 PREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVODGPPQGPP

lerk2     341 NIYY.....................
huHTKL    328 NIYY.....................
AL2.sht   335 NIYY.....................
AL2.long  305 NIYYTSISVLEWPILHTIQLFFNRSKCSRVTTFLFPVOVITTSTCRMTSF

lerk2     345 .....................KV.....................
huHTKL    332 .....................KV.....................
AL2.sht   335 .....................KV.....................
AL2.long  385 SFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALFVLVIILLLGRLNMH

AL2.long  435 CTTLLRDRASVEAEAGOHGPL
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FIGURE 4

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LERK2.1    1  MA·RPGQR····KWLVAMVVWALCRLATPLAKNLEPVSWSLNPKFLSGKG
huHTKL     1  MAVRRDSVWKYCWGVLMV···LCRTAISKSIVLEPIYWNSSNSKFLPGQG
ALII.long  1  MGPPHSGP·GGVRVGALLL··LGVLGLVSGLSLEPVYWNANKRFQAEGG

LERK2.1   50  LVIYPKIGDKLDIICPRA···EAGR··PYEYYKLYLVRPEQAACSTVLD
huHTKL    48  LVLYPQIGDKLDIICPKV···DSKTVGQYEYYKVYMVDKDQADRCTIKKE
ALII.long 48  YVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPA

LERK2.1   95  PNVLVTCNRPEQEIRFTIKFQEFSPNYMGLEFKKHHDYYITSTSNGSLEG
huHTKL    95  NTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNKDYYIISTSNGSLEG
ALII.long 98  PNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG

LERK2.1  145  LENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTTSRPSKEADNTVKMATQ
huHTKL   145  LDNQEGGVCQTRAMKILMKVGQDASS······AGSTRNKDPTRRPELEAG
ALII.long 148 LESLQGGVCLTRGMKVLLRVGQSPR·······GGAVPRKPVSEMPME·R

LERK2.1  195  APGSRGSLGDSDGKHETVNEEKSGPGASGGSSGDPDGFFNSKVALFAAV
huHTKL   189  TNG·RSSTTSPFVKPNPGSSTDGNSAGHSG·····NNILGSEVALFAGI
ALII.long 189 DRGAAHSLEPGKENLPGDPTSNATSRGAEG·······PLPPPSMPAVAGA

LERK2.1  245  GAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQRAAALSL···STLASPKGG
huHTKL   232  ASGCIIFIVIIITLVVLLLKYRRRHRKHSPQHTTTLSL···STLATPKRS
ALII.long 232 AGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGG

LERK2.1  292  S·GTAGTEPSDIIIPLR···TTENNYCPHYEKVSGDYGHPVYIVQEMPPQ
huHTKL   279  G·NNNGSEPSDIIIPLR···TADSVFCPHYEKVSGDYGHPVYIVQEMPPQ
ALII.long 282 GMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQ

LERK2.1  338  SPANIYY·································
huHTKL   325  SPANIYY·································
ALII.long 332 SPPNIYYTSISVLEWPILHTIQLFFMRSKCSRVTTFLFPVQVITTSTCRM

LERK2.1  345  ······························KV···············
huHTKL   332  ······························KV···············
ALII.long 382 TSFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALFVLVLILLLGRL

ALII.long 432 NMHQTTLLRQRASVEAEAGQHGPL
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FIGURE 5